GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 00:15:27 ; Search time 1259 Seconds
(without alignments)
688.531 Million cell updates/sec

Title: US-10-001-863-25
Perfect score: 20
Sequence: 1 ccacaacaatcacctttcgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1599740

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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37: em_htg_vrt:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	17	85.0	20	6	AX057495	AX057495 Sequence
	2	13.6	68.0	30	6	AX792001	AX792001 Sequence
c	3	13.4	67.0	27	6	AR371240	AR371240 Sequence
c	4	13.4	67.0	41	6	AX514287	AX514287 Sequence
c	5	13.4	67.0	41	6	AX520469	AX520469 Sequence
	6	13.2	66.0	19	6	AR270995	AR270995 Sequence
	7	13.2	66.0	36	6	AR123370	AR123370 Sequence
	8	13.2	66.0	42	6	AR261792	AR261792 Sequence
c	9	13	65.0	38	6	AR330200	AR330200 Sequence
	10	13	65.0	45	6	AX598060	AX598060 Sequence
	11	12.8	64.0	17	6	BD255102	BD255102 Regulatio
c	12	12.8	64.0	24	6	AX493101	AX493101 Sequence
	13	12.8	64.0	29	6	AX149586	AX149586 Sequence
c	14	12.6	63.0	25	6	E59922	E59922 Human male-
	15	12.6	63.0	26	6	AX085182	AX085182 Sequence
	16	12.6	63.0	26	6	AX085379	AX085379 Sequence
c	17	12.6	63.0	27	6	AX556427	AX556427 Sequence
c	18	12.6	63.0	28	6	AX085181	AX085181 Sequence
c	19	12.6	63.0	28	6	AX085378	AX085378 Sequence
	20	12.6	63.0	32	6	AX135119	AX135119 Sequence
c	21	12.6	63.0	32	6	AX135120	AX135120 Sequence
	22	12.4	62.0	29	6	BD260451	BD260451 Secreted
c	23	12.4	62.0	41	6	AX521296	AX521296 Sequence
c	24	12.4	62.0	41	8	AJ596568	AJ596568 Arabidops
c	25	12.2	61.0	26	6	BD078213	BD078213 Modulator
	26	12.2	61.0	31	6	AX003697	AX003697 Sequence
	27	12.2	61.0	31	6	AX115943	AX115943 Sequence
	28	12.2	61.0	31	6	AX221284	AX221284 Sequence
	29	12.2	61.0	31	6	AX221379	AX221379 Sequence
	30	12.2	61.0	31	6	BD086097	BD086097 Stress-to
	31	12.2	61.0	36	6	AR177558	AR177558 Sequence
	32	12.2	61.0	36	6	E59074	E59074 Novel carbo
	33	12.2	61.0	36	6	AR217754	AR217754 Sequence
	34	12.2	61.0	36	6	AR256965	AR256965 Sequence
c	35	12.2	61.0	42	6	AX590997	AX590997 Sequence
c	36	12.2	61.0	42	6	AX591150	AX591150 Sequence
c	37	12.2	61.0	42	6	AX717573	AX717573 Sequence
	38	12.2	61.0	43	6	AX484481	AX484481 Sequence
	39	12.2	61.0	45	6	AX467369	AX467369 Sequence
c	40	12.2	61.0	47	6	AX590990	AX590990 Sequence
c	41	12.2	61.0	47	6	AX591143	AX591143 Sequence
c	42	12.2	61.0	47	6	AX717566	AX717566 Sequence
	43	12.2	61.0	48	6	AX014267	AX014267 Sequence
	44	12.2	61.0	48	6	AX839763	AX839763 Sequence
	45	12.2	61.0	48	6	BD205043	BD205043 CD19XCD3-

ALIGNMENTS

RESULT 1
AX057495/c
LOCUS AX057495 20 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 31 from Patent WO0077204.
ACCESSION AX057495
VERSION AX057495.1 GI:12310229
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Lorenz,E., Schwartz,D.A. and Schutte,B.C.
TITLE Variant tlr4 nucleic acid and uses thereof
JOURNAL Patent: WO 0077204-A 31 21-DEC-2000;

```
          University of Iowa Research Foundation (US) ; Lorenz, Eva (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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  Best Local Similarity   100.0%;  Pred. No. 3e+02;
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Qy          4 CAACAATCACCTTTCGG 20
              |||||||||||||||||
Db         20 CAACAATCACCTTTCGG 4


RESULT 2
AX792001
LOCUS       AX792001                  30 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Sequence 4465 from Patent WO02066501.
ACCESSION   AX792001
VERSION     AX792001.1  GI:32957448
KEYWORDS    .
SOURCE      Helicobacter pylori
  ORGANISM  Helicobacter pylori
            Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
            Helicobacteraceae; Helicobacter.
REFERENCE   1
  AUTHORS   Legrain,P., Rain,J.C., Colland,F., de Reuse,H. and Labigne,A.
  TITLE     Protein-protein interactions in Helicobacter pylori
  JOURNAL   Patent: WO 02066501-A 4465 29-AUG-2002;
            Hybrigenics (FR) ; INSTITUT PASTEUR (FR)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Helicobacter pylori"
                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match             68.0%;  Score 13.6;  DB 6;  Length 30;
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  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CCACAACAATCACCTTTCGG 20
              | || || |||||| |||||
Db          1 CTACTACTATCACCCTTCGG 20


RESULT 3
AR371240/c
LOCUS       AR371240                  27 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 47 from patent US 6395472.
ACCESSION   AR371240
VERSION     AR371240.1  GI:34608170
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Leary,T.P., Erker,J., Chalmers,M., Simons,J., Birkenmeyer,L.,
            Muerhoff,S., Pilot-Matias,T., Desai,S. and Mushahwar,I.
  TITLE     Methods of utilizing the TT virus
  JOURNAL   Patent: US 6395472-A 47 28-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
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ORIGIN

  Query Match             67.0%;  Score 13.4;  DB 6;  Length 27;
  Best Local Similarity   93.3%;  Pred. No. 3.1e+04;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCACAACAATCACCT 15
              ||||||||||| |||
Db         23 CCACAACAATCCCCT 9


RESULT 4
AX514287/c
LOCUS       AX514287                  41 bp    DNA     linear   PAT 05-OCT-2002
DEFINITION  Sequence 485 from Patent WO02052044.
ACCESSION   AX514287
VERSION     AX514287.1  GI:23560674
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
  TITLE     Detection of genetic polymorphisms
  JOURNAL   Patent: WO 02052044-A 485 04-JUL-2002;
            Riken (JP)
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             67.0%;  Score 13.4;  DB 6;  Length 41;
  Best Local Similarity   82.4%;  Pred. No. 3.2e+04;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 ACAACAATCACCTTTCG 19
              ||| || |||||||||:
Db         37 ACATCACTCACCTTTCR 21


RESULT 5
AX520469/c
LOCUS       AX520469                  41 bp    DNA     linear   PAT 05-OCT-2002
DEFINITION  Sequence 6667 from Patent WO02052044.
ACCESSION   AX520469
VERSION     AX520469.1  GI:23571067
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
  TITLE     Detection of genetic polymorphisms
  JOURNAL   Patent: WO 02052044-A 6667 04-JUL-2002;
            Riken (JP)
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 ACAACAATCACCTTTCG 19
              ||| || |||||||||:
Db         37 ACATCACTCACCTTTCR 21


RESULT 6
AR270995
LOCUS       AR270995                  19 bp    DNA     linear   PAT 10-APR-2003
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DEFINITION  Sequence 14 from patent US 6501004.
ACCESSION   AR270995
VERSION     AR270995.1  GI:29702254
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Selvaraj,G., Nair,R.B., Joy,R.W. IV, Keller,W.A. and Datla,R.S.
  TITLE     Transgenic reduction of sinapine in crucifera
  JOURNAL   Patent: US 6501004-A 14 31-DEC-2002;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 CCACAACAATCACCTTTC 18
              ||| | ||| ||||||||
Db          1 CCATACCAACCACCTTTC 18


RESULT 7
AR123370
LOCUS       AR123370                 36 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 19 from patent US 6169232.
ACCESSION   AR123370
VERSION     AR123370.1  GI:14108336
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Hey,T.D., Merlo,A.Owens. and Walsh,T.A.
  TITLE     Nucleotide sequences of genes encoding sink protein and uses
            thereof for improving the nutritional quality of feeds
  JOURNAL   Patent: US 6169232-A 19 02-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             66.0%;  Score 13.2;  DB 6;  Length 36;
  Best Local Similarity   83.3%;  Pred. No. 4.1e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCACAACAATCACCTTTC 18
              |||| || ||||| ||||
Db          1 CCACTACTATCACGTTTC 18


RESULT 8
AR261792
LOCUS       AR261792                 42 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 218 from patent US 6322995.
ACCESSION   AR261792
VERSION     AR261792.1  GI:28072932
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Hohmann,H.-P., Humbelin,M., van Loon,A. and Schurter,W.
  TITLE     Riboflavin production
  JOURNAL   Patent: US 6322995-A 218 27-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .42
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ORIGIN

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  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 ACAACAATCACCTTTCGG 20
              | ||  ||||||||||||
Db          1 AAAAACATCACCTTTCGG 18


RESULT 9
AR330200/c
LOCUS       AR330200                 38 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 7602 from patent US 6566127.
ACCESSION   AR330200
VERSION     AR330200.1  GI:33716008
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 7602 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .38
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ORIGIN

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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 AATCACCTTTCGG 20
              |||||||||||||
Db         38 AATCACCTTTCGG 26


RESULT 10
AX598060
LOCUS       AX598060                 45 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 334 from Patent WO0244994.
ACCESSION   AX598060
VERSION     AX598060.1  GI:28398234
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brower,A., Brow,M.A., Cracauer,R.F., Fors,L., Granske,R., de arruda
            Indig,M., Kurensky,D., Luedtke,C., Lukowiak,A.A., Lyamichev,V.,
            Neri,B.P., Reimer,N.D., Roeven,R.T., Skrzypczynski,Z., Ziarno,W.A.,
            Comerford,J., Stump,S. and Viegut,D.D.
  TITLE     Systems and method for detection assay production and sale
  JOURNAL   Patent: WO 0244994-A 334 06-JUN-2002;
            THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

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Qy          5 AACAATCACCTTT 17
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Db          4 AACAATCACCTTT 16


RESULT 11
BD255102
LOCUS       BD255102                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD255102
VERSION     BD255102.1  GI:33064872
KEYWORDS    JP 2002541795-A/2895.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 2895 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/2895
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
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ORIGIN

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Qy          1 CCACAACAATCACCTT 16
              ||||||| | ||||||
Db          1 CCACAACTACCACCTT 16


RESULT 12
AX493101/c
LOCUS       AX493101                 24 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 75 from Patent WO02059355.
ACCESSION   AX493101
VERSION     AX493101.1  GI:23338733
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fieldhouse,D. and Kobler,D.
  TITLE     Polynucleotides for use as tags and tag complements, manufacture
            and use thereof
  JOURNAL   Patent: WO 02059355-A 75 01-AUG-2002;
            TM BIOSCIENCE CORP (CA)
FEATURES                Location/Qualifiers
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                        /db_xref="taxon:32630"
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ORIGIN

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  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 ACAACAATCACCTTTC 18
              |||||||||  |||||
Db         23 ACAACAATCTTCTTTC 8


RESULT 13
AX149586
LOCUS       AX149586                 29 bp    DNA     linear   PAT 31-AUG-2001
DEFINITION  Sequence 10 from Patent WO0136604.
ACCESSION   AX149586
VERSION     AX149586.1  GI:14348020
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Madison,E.L. and Ong,E.O.
  TITLE     Nucleic acids encoding endotheliases, endotheliases and uses
            thereof
  JOURNAL   Patent: WO 0136604-A 10 25-MAY-2001;
            CORVAS INTERNATIONAL, INC. (US)
FEATURES                Location/Qualifiers
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Qy          1 CCACAACAATCACCTT 16
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Db          4 CCACCASWRTCACCYT 19


RESULT 14
E59922/c
LOCUS       E59922                   25 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Human male-dominant expression antigen-2, gene encoding it, and use
            thereof.
ACCESSION   E59922
VERSION     E59922.1  GI:18622732
KEYWORDS    JP 2000316580-A/2.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kondo,M. and Matsukuma,S.
  TITLE     Human male-dominant expression antigen-2, gene encoding it, and use
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            thereof
  JOURNAL   Patent: JP 2000316580-A 2 21-NOV-2000;
            ITO HAM KK
COMMENT     OS   Homo sapiens (human)
            PN   JP 2000316580-A/2
            PD   21-NOV-2000
            PF   30-APR-1999 JP 1999125196
            PR
            PI   MASAAKI KONDO,SHOICHI MATSUKUMA
            PC   C12N15/09,C07K14/47,C07K16/18,C12Q1/68,G01N33/50,G01N33/50, PC
              C12N15/00
            CC
            FH   Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
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ORIGIN

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Qy          1 CCACAACAATCACCTTTCG 19
              || | || |||||||||| |
Db         19 CCTCCACCATCACCTTTTG 1


RESULT 15
AX085182
LOCUS       AX085182                 26 bp    DNA     linear   PAT 09-MAR-2001
DEFINITION  Sequence 32 from Patent WO0112798.
ACCESSION   AX085182
VERSION     AX085182.1  GI:13275274
KEYWORDS    .
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1
  AUTHORS   Loerz,H., Dresselhaus,T., Schreiber,D. and Heuer,S.
  TITLE     Male sterile plants
  JOURNAL   Patent: WO 0112798-A 32 22-FEB-2001;
            Suedwestdeutsche Saatzucht (DE)
FEATURES              Location/Qualifiers
     source           1. .26
                      /organism="Zea mays"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:4577"
ORIGIN

  Query Match             63.0%;  Score 12.6;  DB 6;  Length 26;
  Best Local Similarity   78.9%;  Pred. No. 8.7e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CCACAACAATCACCTTTCG 19
              ||||||| |  |||| |||
Db          1 CCACAACCACAACCTCTCG 19


Search completed: July  2, 2004, 00:36:41
Job time : 1264 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 1, 2004, 23:49:23 ; Search time 199 Seconds
(without alignments)
426.955 Million cell updates/sec

Title: US-10-001-863-25
Perfect score: 20
Sequence: 1 ccacaacaatcacctttcgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 3183836

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	7	ACC83590	Acc83590 Human Tol
	2	18	90.0	21	8	ACC70796	Acc70796 Human Tol
c	3	17	85.0	20	4	AAC84795	Aac84795 Human TLR
c	4	14.2	71.0	50	6	ABZ03575	Abz03575 Human leu
	5	13.8	69.0	37	7	ABZ58775	Abz58775 Nucleotid
	6	13.8	69.0	37	7	ABX11663	Abx11663 PCR prime
c	7	13.8	69.0	41	6	ABZ49885	Abz49885 Human oes
c	8	13.8	69.0	41	6	ABZ43701	Abz43701 Human oes
	9	13.6	68.0	30	6	ABX68238	Novel Hel
c	10	13.4	67.0	27	3	AAA53656	Aaa53656 Second ro
	11	13.2	66.0	19	5	AAC84485	Aac84485 B. napus
	12	13.2	66.0	24	5	AAI65272	Aai65272 Human ATP
c	13	13.2	66.0	27	1	AAN82044	Aan82044 Probe O-A
c	14	13.2	66.0	27	1	AAN82443	Aan82443 Probe O-A
c	15	13.2	66.0	29	1	AAN82043	Aan82043 Probe O-A
	16	13.2	66.0	36	2	AAX78477	Aax78477 Maize RIP
c	17	13.2	66.0	38	6	ABK91081	Abk91081 GST-SOS2
c	18	13.2	66.0	38	6	ABK91083	Abk91083 GST-SOS2
c	19	13.2	66.0	38	6	ABK91076	Abk91076 GST-SOS2
	20	13.2	66.0	42	3	AAZ93754	Putative
	21	13.2	66.0	50	6	ABZ03890	Abz03890 Human leu
	22	12.8	64.0	17	3	AAF02904	Aaf02904 Hammerhea
c	23	12.8	64.0	24	6	ABS61603	Abs61603 Analyte s
	24	12.8	64.0	28	5	AAS15819	Aas15819 Human pro
	25	12.8	64.0	30	6	ABS55098	Abs55098 Plasmodiu
	26	12.8	64.0	31	7	ACD65362	Acd65362 HCV minus
	27	12.8	64.0	34	6	ABS55092	Abs55092 Plasmodiu
c	28	12.8	64.0	50	6	ABZ04718	Abz04718 Human leu
c	29	12.8	64.0	50	6	ABZ02773	Abz02773 Human leu
c	30	12.6	63.0	20	6	ABX03604	Abx03604 Cytochrom
	31	12.6	63.0	24	6	ABS55315	Abs55315 Staphyloc
c	32	12.6	63.0	25	5	AAF32509	Aaf32509 Human mal
c	33	12.6	63.0	25	8	ACI68264	Aci68264 Human mic
	34	12.6	63.0	25	8	ACI31090	Aci31090 Human mic
	35	12.6	63.0	25	8	ACI87613	Aci87613 Human mic
	36	12.6	63.0	26	4	AAF76088	Aaf76088 Maize gen
	37	12.6	63.0	26	5	AAF76475	Aaf76475 Maize ZmM
c	38	12.6	63.0	27	6	ABX08386	Abx08386 Human PDE
c	39	12.6	63.0	28	4	AAF76087	Aaf76087 Maize gen
c	40	12.6	63.0	28	5	AAF76474	Aaf76474 Maize ZmM
	41	12.6	63.0	32	4	AAH20370	Aah20370 Mutagenic
c	42	12.6	63.0	32	4	AAH20371	Aah20371 Mutagenic
c	43	12.6	63.0	50	2	AAZ20917	Aaz20917 Primer fo
c	44	12.6	63.0	50	6	ABZ02336	Abz02336 Human leu
	45	12.6	63.0	50	6	ABZ07468	Abz07468 Human leu

ALIGNMENTS

RESULT 1
ACC83590
ID ACC83590 standard; DNA; 20 BP.
XX
AC ACC83590;
XX
DT 08-SEP-2003 (first entry)
XX
DE Human Toll-like receptor 4 antisense oligonucleotide ISIS #114646.
XX
KW Human; Toll-like receptor 4; receptor; antiinflammatory; immunomodulator;
KW phosphorothioate; antisense; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER = phosphorothioate nucleotides, the
FT oligonucleotide comprises a central gap region of 10 2'-
FT deoxynucleotides, flanked on both sites by 5-nucleotides
FT wings composed of 2'-methoxyethyl nucleotides"
FT modified_base 1
FT /*tag= b
FT /mod_base= m5c
FT modified_base 2
FT /*tag= c
FT /mod_base= m5c
FT modified_base 4
FT /*tag= d
FT /mod_base= m5c
FT modified_base 7
FT /*tag= e
FT /mod_base= m5c
FT modified_base 11
FT /*tag= f
FT /mod_base= m5c
FT modified_base 13
FT /*tag= g
FT /mod_base= m5c
FT modified_base 14
FT /*tag= h
FT /mod_base= m5c
FT modified_base 18
FT /*tag= i

```
FT                   /mod_base= m5c
XX
PN   WO2003044163-A2.
XX
PD   30-MAY-2003.
XX
PF   14-NOV-2002; 2002WO-US036390.
XX
PR   19-NOV-2001; 2001US-00001863.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Karras JG,  Koller E;
XX
DR   WPI; 2003-468766/44.
XX
PT   New antisense oligonucleotides for modulating Toll-like receptor 4 gene
PT   expression, particularly useful for preventing, delaying or treating e.g.
PT   inflammatory disorders, or conditions involving Th1 or Th2 immune
PT   responses.
XX
PS   Claim 3; Page 95; 110pp; English.
XX
CC   The present sequence is that of antisense oligonucleotide ISIS #114646.
CC   This chimeric phosphorothioate oligonucleotide, having 2'-MOE wings and a
CC   deoxy gap, is targeted to the coding region of human Toll-like receptor 4
CC   mRNA. It exhibits 85% inhibition of human Toll-like receptor 4 expression
CC   in THP-1 cells. It is useful for inhibiting the expression of Toll-like
CC   receptor 4 in cells or tissues. The oligonucleotide is particularly
CC   useful for treating or preventing a disease or condition associated with
CC   Toll-like receptor 4, e.g. an inflammatory disorder or a condition
CC   involving an immune response, particularly Th1 or Th2 responses
XX
SQ   Sequence 20 BP; 6 A; 8 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 7;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCACAACAATCACCTTTCGG 20
              ||||||||||||||||||||
Db          1 CCACAACAATCACCTTTCGG 20


RESULT 2
ACC70796
ID   ACC70796 standard; DNA; 21 BP.
XX
AC   ACC70796;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human Toll-like receptor 4, Tlr-4, PCR primer #2.
XX
KW   Human; PCR; primer; vulnerary; anti-tumour; antirheumatic; antiarthritic;
KW   antiarteriosclerotic; cytostatic; neointima; scar; plaque; blood vessel;
KW   Toll-like receptor 4; adventitial cell; Tlr-4; ss.
XX
OS   Homo sapiens.
XX
PN   EP1302206-A1.
XX
PD   16-APR-2003.
XX
PF   11-OCT-2001; 2001EP-00203846.
XX
PR   11-OCT-2001; 2001EP-00203846.
XX
PA   (UYUT-) UNIV UTRECHT MEDISCH CENT.
PA   (UYUT-) RIJKSUNIV UTRECHT.
XX
PI   De Kleijn DPV,  Pasterkamp G;
XX
DR   WPI; 2003-484923/46.
XX
PT   Interfering with the formation of a neointima/scar and/or a plaque in a
PT   blood vessel, useful for modulating tumor growth, comprises providing a
PT   ligand capable of modulating Toll-like receptor activity of adventitial
PT   cells.
XX
PS   Disclosure; Page 7; 23pp; English.
XX
CC   The present invention relates to a method for interfering with the
CC   formation of a neointima/scar and/or a plaque in a blood vessel by
CC   providing a ligand capable of modulating Toll-like receptor activity of
CC   adventitial cells. The method is useful for reducing the formation of a
CC   neointima/scar and/or a plaque in a blood vessel after stenting,
CC   angioplasty, heart transplantation, by pass surgery, arteriovenous
CC   shunting and infection, especially bacterial infection. The method is
CC   also useful for modulating tumour growth, and for modulating the effects
CC   of rheumatoid arthritis. The present sequence is a PCR primer for human
CC   Toll-like receptor 4 (Tlr-4)
XX
SQ   Sequence 21 BP; 8 A; 9 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 18;  DB 8;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCACAACAATCACCTTTC 18
              ||||||||||||||||||
Db          4 CCACAACAATCACCTTTC 21


RESULT 3
AAC84795/c
ID   AAC84795 standard; DNA; 20 BP.
XX
AC   AAC84795;
XX
DT   20-APR-2001  (first entry)
XX
DE   Human TLR4 gene exon 4 amplifying forward primer.
XX
KW   TLR4; toll receptor 4; innate immunity; gram-negative bacteria; sepsis;
KW   respiratory distress syndrome; LPS; lipopolysaccharide; asthma; ARDS;
KW   chronic airway disease; arthritis; inflammatory disease; SIRS; human;
KW   systematic inflammatory response syndrome; pyelonephritis; bronchitis;
KW   acute respiratory distress syndrome; gall bladder disease; pneumonia;
KW   cystic fibrosis; antibacterial; antiinflammatory; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200077204-A1.
XX
PD   21-DEC-2000.
XX
PF   08-JUN-2000; 2000WO-US015723.
XX
PR   10-JUN-1999;   99US-00329515.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (LORE/) LORENZ E.
XX
PI   Lorenz E,  Schwartz DA,  Schutte BC;
XX
DR   WPI; 2001-061872/07.
XX
PT   Identifying humans at risk of, or having indication associated with
PT   altered innate immunity involves detecting or determining whether DNA
PT   amplified from a biological sample encodes a portion of variant toll
PT   receptor 4.
XX
PS   Example 1; Page 31; 97pp; English.
XX
CC   The invention relates to human toll receptor 4 (TLR4) nucleic acid and
```

```
CC   methods to identify polymorphisms at the human TLR4 locus and to identify
CC   individuals at risk of, or having, an indication associated with altered
CC   innate immunity. A variant TLR4 nucleic acid is useful as a diagnostic
CC   reagent for detecting a polymorphism in human TLR4 gene. Since the
CC   presence of TLR4 mutation is associated with gram-negative sepsis,
CC   severity of sepsis, pre-term delivery and respiratory distress syndrome
CC   in pre-term infants, agents which alter TLR4 activity are useful for
CC   preventing or ameliorating infection by gram-negative bacteria, sepsis
CC   induced by gram-negative bacteria, LPS (lipopolysaccharide) induced
CC   chronic airway disease, asthma, arthritis, local and systemic
CC   inflammatory disease conditions such as systematic inflammatory response
CC   syndrome (SIRS) or acute respiratory distress syndrome (ARDS),
CC   pyelonephritis, gall bladder disease, pneumonia, bronchitis, chronic
CC   obstructive pulmonary disease, local gram-negative bacterial infection
CC   and cystic fibrosis. Sequences AAC84776-823 represent PCR primers for
CC   amplifying the exons of human TLR4 gene
XX
SQ   Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match             85.0%;  Score 17;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CAACAATCACCTTTCGG 20
              |||||||||||||||||
Db         20 CAACAATCACCTTTCGG 4


RESULT 4
ABZ03575/c
ID   ABZ03575 standard; DNA; 50 BP.
XX
AC   ABZ03575;
XX
DT   09-JAN-2003  (first entry)
XX
DE   Human leukocyte gene expression profiling probe SEQ ID NO 3566.
XX
KW   T7; leukocyte; gene expression profiling; allograft rejection;
KW   atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW   rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO200257414-A2.
XX
PD   25-JUL-2002.
XX
PF   22-OCT-2001; 2001WO-US047856.
XX
PR   20-OCT-2000; 2000US-0241994P.
PR   08-JUN-2001; 2001US-0296764P.
XX
PA   (BIOC-) BIOCARDIA INC.
XX
PI   Wohlgemuth J,  Fry K,  Matcuk G,  Altman P,  Prentice J,  Phillips J;
PI   Ly N,  Woodward R,  Quertermous T,  Johnson F;
XX
DR   WPI; 2002-636525/68.
XX
PT   New system for leukocyte expression profiling, diagnosing a disease, or
PT   monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT   or congestive heart failure, comprises diagnostic oligonucleotides.
XX
PS   Claim 1; Page 440; 0pp; English.
XX
CC   The invention relates to a system for detecting gene expression, which
CC   comprises one or two isolated DNA molecules that detect expression of a
CC   gene, where the gene corresponds to any of 8143 oligonucleotides
CC   (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC   for leukocyte expression profiling. It is particularly useful for
CC   diagnosing a disease, monitoring (rate of) progression of a disease,
CC   predicting therapeutic outcome, determining prognosis for a patient,
CC   predicting disease complications in an individual or monitoring response
CC   to treatment in an individual. The diseases include cardiac allograft
CC   rejection, kidney allograft rejection, liver allograft rejection,
CC   atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC   rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ   Sequence 50 BP; 10 A; 6 C; 17 G; 17 T; 0 U; 0 Other;

  Query Match             71.0%;  Score 14.2;  DB 6;  Length 50;
  Best Local Similarity   84.2%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCACAACAATCACCTTTCG 19
              ||| |||||||||| ||| |
Db         27 CCAGAACAATCACATTTGG 9


RESULT 5
ABZ58775
ID   ABZ58775 standard; DNA; 37 BP.
XX
AC   ABZ58775;
XX
DT   01-MAY-2003  (first entry)
XX
DE   Nucleotide sequence of oligonucleotide DE09.
XX
KW   Nucleic acid insertion; recombination; nucleic acid selection;
KW   nucleic acid isolation; Fis; ss.
XX
OS   Synthetic.
XX
PN   WO200295055-A2.
XX
PD   28-NOV-2002.
XX
PF   21-MAY-2002; 2002WO-US015947.
XX
PR   21-MAY-2001; 2001US-0291973P.
XX
PA   (INVI-) INVITROGEN CORP.
XX
PI   Brasch MA,  Cheo D,  Li X,  Esposito D,  Byrd DRN;
XX
DR   WPI; 2003-129436/12.
XX
PT   Inserting a population of nucleic acids into a second target molecule for
PT   selecting and isolating nucleic acid molecules by mixing the second
PT   population of nucleic acid with a second target nucleic acid.
XX
PS   Example 8; Page 191; 273pp; English.
XX
CC   The invention relates to inserting a population of nucleic acids into a
CC   second target molecule. The method involves (a) mixing a first population
CC   of nucleic acid comprising one or more recombination sites with a target
CC   nucleic acid; (b) causing some or all of the nucleic acid molecules of
CC   the first population to recombine with the first target nucleic acid
CC   molecules to form a second population; (c) mixing the second population
CC   of nucleic acid with a second target nucleic acid; and (d) causing some
CC   or all of the nucleic acid molecules of the second population to
CC   recombine with some or all of the second target nucleic acid molecules to
CC   form a third population of nucleic acid. The method is useful for
CC   selecting and isolating nucleic acid molecules. Sequences ABZ58775-79
CC   represent oligonucleotides used in the method of the invention
XX
SQ   Sequence 37 BP; 12 A; 9 C; 12 G; 4 T; 0 U; 0 Other;

  Query Match             69.0%;  Score 13.8;  DB 7;  Length 37;
  Best Local Similarity   88.2%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 ACAACAATCACCTTTCG 19
```

```
                    |||| |||||||||| ||
Db          20 ACAAAAATCACCTTGCG 36


RESULT 6
ABX11663
ID   ABX11663 standard; DNA; 37 BP.
XX
AC   ABX11663;
XX
DT   06-MAY-2003  (first entry)
XX
DE   PCR primer DE09 used to amplify Bacteriophage lambda attP sequence.
XX
KW   Recombinational cloning; nucleic acid; recombination protein;
KW   Fis protein; recombination system; attP; PCR; primer; ss.
XX
OS   Bacteriophage lambda.
XX
PN   WO200286144-A2.
XX
PD   31-OCT-2002.
XX
PF   19-APR-2002; 2002WO-US012331.
XX
PR   19-APR-2001; 2001US-0284528P.
XX
PA   (INVI-) INVITROGEN CORP.
XX
PI   Byrd DRN,  Esposito D;
XX
DR   WPI; 2003-093145/08.
XX
PT   New composition for recombinational cloning of nucleic acid molecules,
PT   comprises at least one recombination protein and at least one Fis protein
PT   or its fragment.
XX
PS   Example 3; Page 97; 144pp; English.
XX
CC   The present invention relates to compositions and methods for the
CC   recombinational cloning of nucleic acids. The compositions comprise at
CC   least one recombination protein and at least one Fis protein or its
CC   fragment, where the recombination protein is present in an amount for
CC   recombinational cloning of at least one nucleic acid molecule, and the
CC   Fis protein or its fragment is present in an amount for enhancing the
CC   efficiency of the recombinational cloning. The compositions and methods
CC   of the invention are useful in the recombinational cloning of nucleic
CC   acid molecules using recombination systems. The present sequence
CC   represents a PCR primer used to amplify Bacteriophage lambda attP
CC   sequence in the examples of the present invention
XX
SQ   Sequence 37 BP; 12 A; 9 C; 12 G; 4 T; 0 U; 0 Other;

  Query Match             69.0%;  Score 13.8;  DB 7;  Length 37;
  Best Local Similarity   88.2%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           3 ACAACAATCACCTTTCG 19
                 |||| |||||||||| ||
Db          20 ACAAAAATCACCTTGCG 36


RESULT 7
ABZ49885/c
ID   ABZ49885 standard; DNA; 41 BP.
XX
AC   ABZ49885;
XX
DT   26-JUN-2003  (first entry)
XX
DE   Human oestrogen sulphotransferase STE gene polymorphic site, #6667.
XX
KW   Human; drug metabolising enzyme; gene; drug metabolism; chromosome 4;
KW   polymorphic site; drug evaluation; drug screening; genotyping;
KW   genetic profiling; therapeutic customisation; adverse reaction;
KW   clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(21,T)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN   WO200252044-A2.
XX
PD   04-JUL-2002.
XX
PF   27-DEC-2001; 2001WO-JP011592.
XX
PR   27-DEC-2000; 2000JP-00399443.
PR   02-MAY-2001; 2001JP-00135256.
PR   27-AUG-2001; 2001JP-00256862.
XX
PA   (RIKE ) RIKEN KK.
XX
PI   Nakamura Y,  Sekine A,  Iida A,  Saito S;
XX
DR   WPI; 2002-583571/62.
XX
PT   Identifying individuals having a polymorphism, useful for determining the
PT   effectiveness or side effect of a drug or treatment protocol, comprises
PT   detecting at least one polymorphism in the drug metabolizing enzyme
PT   nucleic acid.
XX
PS   Claim 23; Page 200; 2785pp; English.
XX
CC   Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
CC   encoding enzymes associated with drug metabolism. The invention relates
CC   to methods and compositions for identifying individuals who have at least
CC   one polymorphism in such drug metabolising enzyme-encoding genes. The
CC   polymorphisms may be identified in a nucleic acid sample using probes or
CC   primers specific for a sequence selected from ABZ43217-ABZ50887 using a
CC   variety of detection assays, including hybridisation assays, nucleic acid
CC   arrays and PCR-based methods. The invention also encompasses methods of
CC   evaluating and screening drugs using genetic polymorphism data. Genetic
CC   polymorphism data, particularly that relating to single nucleotide
CC   polymorphisms (SNPs), may be used in studying the relationship between
CC   DNA sequence variations and human diseases, conditions, and responses to
CC   drugs. SNPs are also useful as polymorphism markers for discovering genes
CC   that cause or exacerbate certain diseases. SNPs are particularly useful
CC   in the above respects as they are stable in populations, occur
CC   frequently, and have lower mutation rates than other genome variations
CC   such as repeating sequences. The detection and analysis of polymorphisms
CC   in genes encoding drug metabolising enzymes allows the customisation of
CC   drug therapies based upon the genetic profile of individual patients.
CC   This would not only take the guesswork out of selecting the drug with the
CC   greatest therapeutic effect for a particular patient, but would also
CC   reduce the likelihood of adverse reactions, thereby increasing safety.
CC   Methods of the invention are also useful in the drug discovery and
CC   approval processes. For example, individuals could be selected for
CC   clinical trials only if their genetic profiles indicate that they are
CC   capable of responding to a particular drug or drug class, and previously
CC   failed drug candidates could be revived if they were matched with more
CC   appropriate patient populations. The methods, data and compositions of
CC   the invention may therefore lead to a an increase in the range of
CC   possible drug targets and decreases in the number of adverse drug
CC   reactions, failed drug trials, the time taken for a drug to be approved,
CC   the length of time patients are on medication and the number of different
CC   medications a patient needs to take before finding an effective therapy
XX
SQ   Sequence 41 BP; 15 A; 4 C; 9 G; 13 T; 0 U; 0 Other;

  Query Match             69.0%;  Score 13.8;  DB 6;  Length 41;
  Best Local Similarity   88.2%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy          3 ACAACAATCACCTTTCG 19
              ||| || ||||||||||
Db         37 ACATCACTCACCTTTCG 21


RESULT 8
ABZ43701/c
ID   ABZ43701 standard; DNA; 41 BP.
XX
AC   ABZ43701;
XX
DT   26-JUN-2003  (first entry)
XX
DE   Human oestrogen sulphotransferase STE gene polymorphic site, #485.
XX
KW   Human; drug metabolising enzyme; gene; drug metabolism; chromosome 4;
KW   polymorphic site; drug evaluation; drug screening; genotyping;
KW   genetic profiling; therapeutic customisation; adverse reaction;
KW   clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(21,T)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN   WO200252044-A2.
XX
PD   04-JUL-2002.
XX
PF   27-DEC-2001; 2001WO-JP011592.
XX
PR   27-DEC-2000; 2000JP-00399443.
PR   02-MAY-2001; 2001JP-00135256.
PR   27-AUG-2001; 2001JP-00256862.
XX
PA   (RIKE ) RIKEN KK.
XX
PI   Nakamura Y,  Sekine A,  Iida A,  Saito S;
XX
DR   WPI; 2002-583571/62.
XX
PT   Identifying individuals having a polymorphism, useful for determining the
PT   effectiveness or side effect of a drug or treatment protocol, comprises
PT   detecting at least one polymorphism in the drug metabolizing enzyme
PT   nucleic acid.
XX
PS   Claim 23; Page 72; 2785pp; English.
XX
CC   Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
CC   encoding enzymes associated with drug metabolism. The invention relates
CC   to methods and compositions for identifying individuals who have at least
CC   one polymorphism in such drug metabolising enzyme-encoding genes. The
CC   polymorphisms may be identified in a nucleic acid sample using probes or
CC   primers specific for a sequence selected from ABZ43217-ABZ50887 using a
CC   variety of detection assays, including hybridisation assays, nucleic acid
CC   arrays and PCR-based methods. The invention also encompasses methods of
CC   evaluating and screening drugs using genetic polymorphism data. Genetic
CC   polymorphism data, particularly that relating to single nucleotide
CC   polymorphisms (SNPs), may be used in studying the relationship between
CC   DNA sequence variations and human diseases, conditions, and responses to
CC   drugs. SNPs are also useful as polymorphism markers for discovering genes
CC   that cause or exacerbate certain diseases. SNPs are particularly useful
CC   in the above respects as they are stable in populations, occur
CC   frequently, and have lower mutation rates than other genome variations
CC   such as repeating sequences. The detection and analysis of polymorphisms
CC   in genes encoding drug metabolising enzymes allows the customisation of
CC   drug therapies based upon the genetic profile of individual patients.
CC   This would not only take the guesswork out of selecting the drug with the
CC   greatest therapeutic effect for a particular patient, but would also
CC   reduce the likelihood of adverse reactions, thereby increasing safety.
CC   Methods of the invention are also useful in the drug discovery and
CC   approval processes. For example, individuals could be selected for
CC   clinical trials only if their genetic profiles indicate that they are
CC   capable of responding to a particular drug or drug class, and previously
CC   failed drug candidates could be revived if they were matched with more
CC   appropriate patient populations. The methods, data and compositions of
CC   the invention may therefore lead to a an increase in the range of
CC   possible drug targets and decreases in the number of adverse drug
CC   reactions, failed drug trials, the time taken for a drug to be approved,
CC   the length of time patients are on medication and the number of different
CC   medications a patient needs to take before finding an effective therapy
XX
SQ   Sequence 41 BP; 15 A; 4 C; 9 G; 13 T; 0 U; 0 Other;

  Query Match             69.0%;  Score 13.8;  DB 6;  Length 41;
  Best Local Similarity   88.2%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 ACAACAATCACCTTTCG 19
              ||| || ||||||||||
Db         37 ACATCACTCACCTTTCG 21


RESULT 9
ABX68238
ID   ABX68238 standard; DNA; 30 BP.
XX
AC   ABX68238;
XX
DT   07-MAY-2003  (first entry)
XX
DE   Novel Helicobacter pylori gene PCR primer #1209.
XX
KW   Protein-protein interaction; ulcer; selected interacting domain; SID;
KW   PCR; primer; ss.
XX
OS   Helicobacter pylori.
XX
PN   WO200266501-A2.
XX
PD   29-AUG-2002.
XX
PF   28-DEC-2001; 2001WO-EP015428.
XX
PR   02-JAN-2001; 2001US-0259302P.
XX
PA   (HYBR-) HYBRIGENICS.
PA   (INSP ) INST PASTEUR.
XX
PI   Legrain P,  Rain J,  Colland F,  De Reuse H,  Labigne A;
XX
DR   WPI; 2002-674910/72.
XX
PT   New complexes of protein-protein interactions in Helicobacter pylori,
PT   useful for identifying modulating compounds for treating or preventing
PT   ulcers in mammals.
XX
PS   Example 9; Page 525; 642pp; English.
XX
CC   The invention describes a complex of protein-protein interactions in
CC   Helicobacter pylori selected from 421 complexes given in the
CC   specification. The complex of protein-protein interactions are useful for
CC   screening for agents which modulate the interaction of proteins.
CC   Modulating compounds which binds to a targeted bacterial protein may be
CC   used for treating or preventing ulcers in a human or animal. This
CC   sequence represents a primer used to isolate polynucleotides encoding
CC   Helicobacter pylori proteins for studies on protein-protein interactions
XX
SQ   Sequence 30 BP; 6 A; 9 C; 4 G; 8 T; 3 U; 0 Other;

  Query Match             68.0%;  Score 13.6;  DB 6;  Length 30;
  Best Local Similarity   80.0%;  Pred. No. 4.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
Qy          1 CCACAACAATCACCTTTCGG 20
              | || || |||||| |||||
Db          1 CUACUACUATCACCCTTCGG 20
```

RESULT 10
AAA53656/c
ID AAA53656 standard; DNA; 27 BP.
XX
AC AAA53656;
XX
DT 15-SEP-2003 (revised)
DT 04-DEC-2000 (first entry)
XX
DE Second round antisense primer ufttv2c-2 for TTV US35 genome.
XX
KW TTV; TT virus; blood transmission; detection; amplification; primer;
KW transplantation; xenotransplantation; vector; ss.
XX
OS TT virus; isolate US35.
XX
PN WO200046407-A2.
XX
PD 10-AUG-2000.
XX
PF 04-FEB-2000; 2000WO-US002982.
XX
PR 05-FEB-1999; 99US-00245248.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Leary TP, Simons JN, Erker JC, Chalmers ML, Birkenmeyer LG;
PI Muerhoff AS, Pilot-Matias TJ, Desai SM, Mushahwar IK;
XX
DR WPI; 2000-514969/46.
XX
PT New oligomer primer useful for the detection of TT virus in test samples
PT and tissues and organs for use in (xeno)transplantation.
XX
PS Example 6.1; Page 106; 139pp; English.
XX
CC Primers shown in AAA53645-56 were used for the construction of full or
CC near full length TT virus (TTV) genomes (see AAA53637-44) in attempt to
CC more fully understand the TTV genome. Previously, of the hundreds of TTV
CC isolates, only one full length TTV (isolate GH1 - see AAA53632) and two
CC near full length isolates (TA278 and TTV CHN1) have been reported. TTV is
CC a circular, negative single-stranded DNA virus. Isolate GH1 was 3852
CC nucleotides in length, 113 nucleotides longer than previously reported.
CC The newly discovered region is GC rish (89 percent) and contains several
CC potential stem-loop structures. TTV DNA can be transmitted by blood or
CC blood products. It is also possible that TTV is transmitted by a faecal-
CC oral route, demonstrated by the presence of TTV in the faeces of infected
CC humans. Detection of TTV in test samples can be enhanced by use of DNA
CC amplification assays that use DNA oligomers as primers. The primers are
CC useful for detecting the presence of TTV target nucleotides in biological
CC samples and tissues and organs to be used in transplantation and
CC xenotransplantation (claimed). The TTV genome itself can be used as a
CC vector in order to introduce heterologous DNA into a host cell. (Updated
CC on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 27 BP; 4 A; 4 C; 9 G; 10 T; 0 U; 0 Other;

```
  Query Match             67.0%;  Score 13.4;  DB 3;  Length 27;
  Best Local Similarity   93.3%;  Pred. No. 5.6e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCACAACAATCACCT 15
              ||||||||||| |||
Db         23 CCACAACAATCCCCT 9
```

RESULT 11
AAC84485
ID AAC84485 standard; DNA; 19 BP.
XX
AC AAC84485;
XX
DT 02-APR-2001 (first entry)
XX
DE B. napus BNF5H1 gene specific primer #4.
XX
KW Crucifera; CYP84 monooxygenase enzyme; CME; ferulate-5 hydroxylase; F5H;
KW enzyme; sinapine; BNF5H1; BNF5H2; BNF5H3; canola; seed meal; lignin;
KW PCR primer; ss.
XX
OS Brassica napus.
XX
PN CA2305864-A1.
XX
PD 06-NOV-2000.
XX
PF 05-MAY-2000; 2000CA-02305864.
XX
PR 06-MAY-1999; 99CA-02270417.
PR 06-MAY-1999; 99US-0132800P.
XX
PA (NAIR/) NAIR R B.
PA (JOYR/) JOY R W.
PA (KELL/) KELLER W A.
PA (DATL/) DATLA R S.
PA (SELV/) SELVARAJ G.
XX
PI Nair RB, Joy RW, Keller WA, Datla RS, Selvaraj G;
XX
DR WPI; 2001-071652/09.
XX
PT Transformed cruciferae plants containing an exogenous DNA sequence
PT encoding antisense equivalents of ferulate 5-hydroxylase, and having
PT reduced sinapine content in seeds than plants of same species.
XX
PS Example; Page 32; 96pp; English.
XX
CC The invention relates to a transformed plant, of the crucifera family
CC containing an exogenous DNA sequence which encodes exogenous CYP84
CC monooxygenase enzyme (CME), particularly a ferulate-5 hydroxylase (F5H)
CC enzyme or antisense equivalent. The transformed plant has a reduced
CC content of sinapine in seeds compared to vector control plants. Three
CC specific nucleic acid sequences encoding Brassica napus F5H polypeptide
CC are disclosed, designated BNF5H1, BNF5H2 and BNF5H3. The transformed
CC plant (preferably canola) is useful for producing seed meal which
CC involves harvesting seeds from the plant and processing the seeds to form
CC seed meal. Down-regulation of the F5H genes in B. napus and other
CC crucifers has a favorable impact on lignin composition and meal
CC digestibility. Sequences AAC84482-85 represent PCR primers specific for
CC BNF5H1 gene
XX
SQ Sequence 19 BP; 5 A; 10 C; 0 G; 4 T; 0 U; 0 Other;

```
  Query Match             66.0%;  Score 13.2;  DB 5;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 6.8e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCACAACAATCACCTTTC 18
              ||| | ||| ||||||||
Db          1 CCATACCAACCACCTTTC 18
```

RESULT 12
AAI65272
ID AAI65272 standard; DNA; 24 BP.
XX
AC AAI65272;
XX
DT 29-NOV-2001 (first entry)
XX

DE Human ATP-dependent serine protease 11-4 PCR primer 2.
XX
KW Human; ATP-dependent serine protease 11.4; cytostatic; virucidal;
KW immunomodulator antiinflammatory; haemostatic; cancer; haemopathy;
KW human immunodeficiency virus; HIV; infection; immunological disease;
KW inflammatory disorder; mitochondrial disease; congenital abnormality;
KW metabolic disturbance disorder; growth disturbance disorder; PCR primer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200172988-A1.
XX
PD 04-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-CN000457.
XX
PR 28-MAR-2000; 2000CN-00115247.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-597121/67.
XX
PT New polypeptide for the diagnosis of malignant neoplasm, hemopathy, HIV
PT infection, immunological diseases and inflammations, comprises the human
PT ATP-dependent serine protease 11.4 protein.
XX
PS Example 2; Page 17; 36pp; Chinese.
XX
CC The invention relates to an isolated polypeptide of human ATP-dependent
CC serine protease 11.4 comprising a sequence of 103 amino acids or its
CC fragment, analogue or derivative. The polypeptide is useful in the
CC diagnosis and treatment of malignant neoplasm, haemopathy, HIV infection,
CC immunological diseases, various inflammatory disorders, mitochondrial
CC disease, energy and substance metabolism-related metabolic disturbance
CC disorder, growth disturbance disorder and congenital abnormality. The
CC present sequence is a primer used to isolate a polynucleotide encoding
CC the polypeptide of the invention
XX
SQ Sequence 24 BP; 11 A; 9 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 5; Length 24;
Best Local Similarity 83.3%; Pred. No. 7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCACAACAATCACCTTTC 18
||||||.|.|||.|||||
Db 4 CCACAAAACTCAACTTTC 21

RESULT 13
AAN82044/c
ID AAN82044 standard; DNA; 27 BP.
XX
AC AAN82044;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 12-DEC-1990 (first entry)
XX
DE Probe O-AY-27 for human genomic DNA.
XX
KW Synthetic oligonucleotide; probe O-AY-27; ss DNA; human genomic DNA.
XX
OS Homo sapiens.
XX
PN EP294098-A.
XX
PD 07-DEC-1988.
XX
PF 26-MAY-1988; 88EP-00304763.
XX
PR 29-MAY-1987; 87US-00055224.
PR 17-MAY-1988; 88US-00194982.
XX
PA (CITY) CITY OF HOPE NAT MEDICAL CENT.
XX
PI Wallace RB;
XX
DR WPI; 1988-347751/49.
XX
PT New oligo-nucleotide hybridisation probe specific for repeat units - with
PT high specificity for single locus, useful e.g. in paternity testing.
XX
PS Claim 7; Page 6; 9pp; English.
XX
CC The probe is used for genetic identification of a sample of human genomic
CC DNA, e.g. for paternity testing, diagnosing cancer or genetic diseases,
CC and studying bone marrow transplant chimerism. Under high criteria it
CC yielded locus-specific or multi-loci, polymorphic hybridisation pattern,
CC and is more specific for a single locus (or small number of loci) than
CC known probes. (Updated on 31-OCT-2002 to add missing OS field.) (Updated
CC on 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct
CC PA field.)
XX
SQ Sequence 27 BP; 6 A; 1 C; 11 G; 2 T; 0 U; 7 Other;

Query Match 66.0%; Score 13.2; DB 1; Length 27;
Best Local Similarity 66.7%; Pred. No. 7.1e+03;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCACAACAATCACCTTTC 18
||||| :: :|:||||||
Db 25 CCACABYRCYCRCCTTTC 8

RESULT 14
AAN82443/c
ID AAN82443 standard; DNA; 27 BP.
XX
AC AAN82443;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 12-DEC-1990 (first entry)
XX
DE Probe O-AY-27 for human genomic DNA.
XX
KW Synthetic oligonucleotide; probe O-AY-27; ss DNA; human genomic DNA.
XX
OS Homo sapiens.
XX
PN EP294098-A.
XX
PD 07-DEC-1988.
XX
PF 26-MAY-1988; 88EP-00304763.
XX
PR 29-MAY-1987; 87US-00055224.
PR 17-MAY-1988; 88US-00194982.
XX
PA (CITY) CITY OF HOPE NAT MEDICAL CENT.
XX
PI Wallace RB;
XX
DR WPI; 1988-347751/49.
XX
PT New oligo-nucleotide hybridisation probe specific for repeat units - with
PT high specificity for single locus, useful e.g. in paternity testing.
XX
PS Claim 7; Page 6; 9pp; English.
XX
CC The probe is used for genetic identification of a sample of human genomic
CC DNA, e.g. for paternity testing, diagnosing cancer or genetic diseases,

CC and studying bone marrow transplant chimerism. Under high criteria it
CC yielded locus-specific or multi-loci, polymorphic hybridisation pattern,
CC and is more specific for a single locus (or small number of loci) than
CC known probes. R=A or G. (Updated on 31-OCT-2002 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
SQ Sequence 27 BP; 6 A; 1 C; 11 G; 2 T; 0 U; 7 Other;

Query Match 66.0%; Score 13.2; DB 1; Length 27;
Best Local Similarity 66.7%; Pred. No. 7.1e+03;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 CCACAACAATCACCTTTC 18
              ||||| :: :|:||||||
Db         25 CCACABYRCYCRCCTTTC 8
```

RESULT 15
AAN82043/c
ID AAN82043 standard; DNA; 29 BP.
XX
AC AAN82043;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 12-DEC-1990 (first entry)
XX
DE Probe O-AY-29 for human genomic DNA.
XX
KW Synthetic oligonucleotide; probe O-AY-29; ss DNA; human genomic DNA.
XX
OS Homo sapiens.
XX
PN EP294098-A.
XX
PD 07-DEC-1988.
XX
PF 26-MAY-1988; 88EP-00304763.
XX
PR 29-MAY-1987; 87US-00055224.
PR 17-MAY-1988; 88US-00194982.
XX
PA (CITY) CITY OF HOPE NAT MEDICAL CENT.
XX
PI Wallace RB;
XX
DR WPI; 1988-347751/49.
XX
PT New oligo-nucleotide hybridisation probe specific for repeat units - with
PT high specificity for single locus, useful e.g. in paternity testing.
XX
PS Claim 7; Page 6; 9pp; English.
XX
CC The probe is used for genetic identification of a sample of human genomic
CC DNA, e.g. for paternity testing, diagnosing cancer or genetic diseases,
CC and studying bone marrow transplant chimerism. Under high criteria it
CC yielded locus-specific or multi-loci, polymorphic hybridisation pattern,
CC and is more specific for a single locus (or small number of loci) than
CC known probes. R=A and/or G, Y=C and/or T, and V=not T. (Updated on 31-OCT
CC -2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PD
CC field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 29 BP; 6 A; 1 C; 13 G; 2 T; 0 U; 7 Other;

Query Match 66.0%; Score 13.2; DB 1; Length 29;
Best Local Similarity 66.7%; Pred. No. 7.1e+03;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 CCACAACAATCACCTTTC 18
              ||||| :: :|:||||||
Db         26 CCACABYRCYCRCCTTTC 9
```

Search completed: July 2, 2004, 00:15:11
Job time : 206 secs